

FT	NP-BIND	66	70	GTP (By similarity).
FT	NP-BIND	124	127	GTP (By similarity).
FT	DOMAIN	40	48	Effector region (By similarity).
FT	LIPID	204	204	S-geranylgeranyl cysteine.
FT	LIPID	205	205	S-geranylgeranyl cysteine.
SRQ	SEQUENCE	205 AA:	22678 MN:	8248FAE3B0E317D6 CRC64;
QY	1	MSNNPENYDYLFLKULLIGDGVGKSCLLRFAADDTYTESYISTIGVDFKIRTEFLDGKUT	60	-ESPNVVKOMQEDRYKASENTVNL 88
QY	1	MSSNAPEDYLFLKULLIGDGVGKSCLLRFAADDTYTESYISTIGVDFKIRTEFLDGKUT	60	-ESPNVVKOMQEDRYKASENTVNL 88
Db	61	KLQI-----	149	181 TAGGAEKSNVKIYSTPVQSGGGCC 205
QY	61	KLQIWDTAGQERTTTSYVYRGAHGLIVWYDVTDQEENVNQWMLQDIDRYSENVNL	120	181 TAGGAEKSNVKIYSTPVQSGGGCC 205
RESULT 2				
RB1A_HUMAN				
ID	-RB1A_HUMAN	STANDARD;	PRT;	205 AA.
AC	P62820;	PI1476;	Q9Y3T2;	
DT	01-OCT-1989	(Rel. 12, Created)		
DT	01-OCT-189	(Rel. 12, Last sequence update)		
DT	01-OCT-2004	(Rel. 45, Last annotation update)		
DE	Ras-related protein Rab-1A (YPT1-related protein).			
GN	Name=RAB1A, Synonyms=RAB1,			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9605;			
[1]	SEQUENCE FROM N.A. (ISOFORM 1).			
RR	MEDLINE=89308688; PubMed=2501306;			
RR	Zahrour A., Touchet N., Chardin P., Tavitian A.;			
RR	The human Rab genes encode a family of GTP-binding proteins related			
RT	to yeast YPT1 and SEC4 products involved in secretion.;			
RT	J. Biol. Chem. 264:12394-12401(1989).			
[2]	SEQUENCE FROM N.A. (ISOFORM 3).			
RR	MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;			
RR	Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,			
RR	Ansorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,			
RR	Laufer J., Duesterhoeft A., Beyer A., Koehrer K., Stracke R.,			
RR	Mewes H.-W., Ottewaelder B., Obermaier B., Tampe J., Heubner D.,			
RR	Wambutt R., Klein B., Klein M., Poustka A.;			
RT	Towards a catalog of human genes and proteins: sequencing and			
RT	analysis of 500 novel complete protein coding human cDNAs.;			
RR	Genome Res. 11:422-435(2001).			
[3]	SEQUENCE FROM N.A. (ISOFORM 1).			
RR	MEDLINE=14702039; DOI=10.1038/ng1285;			
RR	Ota T., Suzuki Y., Nishikawa T., Ottuki T., Sugiyama T., Irie R.,			
RR	Wakamatsu A., Hayashi K., Sato H., Naiji K., Kimura K., Makita H.,			
RR	Sokine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RR	Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,			
RR	SEQUENCE FROM N.A. (ISOFORM 2).			
RR	MEDLINE=91218852; PubMed=1902353;			
RR	Bailly E., McCaffrey M., Touchet N., Zahrour A., Goud B., Bornens M.,			
RR	"Phosphorylation of two small GTP-binding proteins of the Rab family			
RR	by p34dc2.,"			
RR	Nature 350:715-718(1991).			
RR	-!- FUNCTION: Probably required for transit of protein from the ER			
RR	through Golgi compartment. Binds GTP and GDP and possesses			
RR	intrinsic GTPase activity.			
-!- SUBCELLULAR LOCATION: Golgi.				
-!- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=3;			
CC	Name=1;			
CC	Isoform=62820-1 PI1476-1 Sequence=62820-1.			

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OM protein - protein search, using SW model

Run on: November 17, 2004, 14:08:40 ; Search time 38 Seconds
(without alignments)
438.039 Million cell updates/sec

Title: US-09-820-003C-2
Perfect score: 886
Sequence: 1 MSSANPEVDYFLKLLLGDS..... EKSNVRIQSTPVKQSGGGCC 173

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 293416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description

1	850	97.1	205	1	TVDGYP
2	850	97.1	205	1	TVHUYP
3	850	97.1	205	1	TVMSYP
4	849	95.8	205	1	TVRTYP
5	812.5	91.7	201	2	D38625
6	771.5	87.1	201	2	S06147
7	733	82.7	205	2	S38339
8	671	75.7	202	2	JE0310
9	660	74.5	205	2	T33781
10	658.5	74.3	203	2	S30096
11	646.5	73.0	203	2	T50323
12	646.5	73.0	203	2	JC4105
13	642.5	72.5	203	2	JC1247
14	631.5	71.3	201	2	JC5337
15	627.5	70.8	203	2	S34253
16	623.5	70.4	206	2	S04590
17	619.5	69.9	258	2	B9153
18	619	69.9	202	2	S41430
19	618.5	69.8	203	2	S38202
20	613.5	69.2	202	2	S38740
21	612	69.1	221	2	H71444
22	598	67.5	218	2	T07609
23	590.5	66.6	202	2	S72515
24	587	66.3	201	2	S39565
25	574	64.8	206	2	T14391
26	572.5	64.6	195	2	PS0279
27	571	64.4	206	1	TVBYQ
28	523	59.0	208	2	A38202
29	468.5	52.9	208	2	A34716

30 461 52.0 203 2 B34716 GTP-binding protein
31 447 50.5 216 2 T48378 GTP-binding protein
32 442 49.9 215 2 T14365 GTP-binding protein
33 439.5 49.5 215 2 S57478 GTP-binding protein
34 438.5 49.5 216 2 JS0640 GTP-binding protein
35 435.5 49.2 200 2 S12790 GTP-binding protein
36 430.5 48.6 215 2 S57462 GTP-binding protein
37 429.5 48.5 216 2 S57471 GTP-binding protein
38 429.5 48.5 222 2 T14405 small GTP-binding protein
39 428.5 48.4 216 2 T45001 GTPase ARAB8 - Ar
40 426.5 48.1 215 2 S57474 GTP-binding protein
41 425.0 48.0 216 2 B49847 GTP-binding protein
42 418 47.2 207 2 B36364 GTP-binding protein
43 418 47.2 207 2 B36364 GTP-binding protein
44 410.5 46.3 206 2 T17851 GTP-binding protein
45 409.5 46.2 209 2 B38625 GTP-binding protein

RESULT 1

TVOCYP
GTP-binding protein Rab1 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 19-Feb-1994 #Sequence revision 06-Dec-1996 #text_change 19-Jan-2001
C;Accession: S19104; A36364; S1600
R;Serial, M.
Submitted to the EMBL Data Library, August 1990

A;Reference number: S19104
A;Accession: S19104
A;Molecule type: mRNA

A;Title: Molecular cloning of YP1/SEC4-related cDNAs from an epithelial cell line.
A;Reference number: A36364
A;Accession: A36364
A;Strain: nucleic acid sequence not shown

A;Molecule type: mRNA
A;Residues: 1-157, 'BK' 160-205 <CHA>

A;Cross references: GB:X56384; NID:913

C;Function:

A;Description: probably involved in protein transport from the endoplasmic reticulum through the Golgi apparatus; GTP binding; lipoprotein; membrane protein

C;Keywords: endoplasmic reticulum; Golgi apparatus; GTP binding; lipoprotein; membrane protein

GTP-binding protein

F;12-127/Domain: translation elongation factor Tu homology <ERU>
F;18-25/Region: nucleotide-binding motif A (P-loop)

F;62-67/Region: nucleotide-binding motif B

F;124-127/Region: GTP-binding NQX3 motif

F;154-156/Region: GTP-binding SAK/L motif

F;24, 25, 43, 124, 125, 127, 154/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #status predicted

F;194/Binding site: phosphate (Ser) (covalent) (by cdcc kinase) #status predicted

F;204, 205/Binding site: geranyl-geranyl (Cys) (covalent) #status Predicted

Query Match 97.1%; Score 860; DB 1; Length 205;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Matches 173; Conservativity 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Best Local Similarity 84.4%; Pred. No. 1.7e-61; Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MSSANPEVDYFLKLLLGDSGVKSCULLRADDTYFESYVISTIGVPRKIRTELDGKTI 60
Db 1 MSSANPEVDYFLKLLLGDSGVKSCULLRADDTYFESYVISTIGVPRKIRTELDGKTI 60

QY 61 KLOI-----ESFNNVYQWLBIDYASENTNKL 88

QY 149 TAGGAEKSNTKIQSTPVKQSGGGCC 173
 Db 181 TAGGAEKSNTKIQSTPVKQSGGGCC 205

RESULT 2

TVHQP GTP-binding protein Rab1 - human
 N;Alternate names: protein Rab1; ras-related protein ypt1; transforming protein ypt1
 C;Species: Homo sapiens (man)
 C;Date: 29-Jun-1990 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
 C;Accession: A34323; T08598
 R;Zahrour, A.; Touchot, N.; Chardin, P.; Tavitian, A.
 J. Biol. Chem. 264, 12394-12401, 1989
 A;Title: The human Rab genes encode a family of GTP-binding proteins related to yeast YPT1
 A;Reference number: A34323; MUID:89308668; PMID:2501306

A;Accession: A34323
 A;Molecule type: mRNA
 A;Residues: 1-205 <ZAH>
 A;Cross-references: UNIPROT:PI1476; GB:J04941; GB:MB28209; NID:9550059; PIDN:AAA60240.1;
 A;Experimental source: pheochromocytoma
 R;Mambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, March 1999

A;Reference number: Z16471
 A;Accession: T08698
 A;Cross-references: mRNA
 A;Residues: 1-64-141-205 <WAN>
 A;Cross-references: EMBL:ALU50268
 A;Experimental source: fetal brain; clone DKFZP564B163
 C;Genetics:

A;Gene: GDB:RAB1
 A;Cross-references: GDB:118857; OMIM:179508
 A;Map position: 4p15.31-4p15.31
 A;Note: DKFZP564B163.1

A;C;Function:

A;Description: probably involved in protein transport from the endoplasmic reticulum through the Golgi apparatus; GTP binding; membrane protein
 C;Keywords: endoplasmic reticulum; Golgi apparatus; GTP binding; lipoprotein; membrane protein

F1-205/Region: GTP-binding protein Rab1 #status predicted <MAT1>
 F1-64,141-205/Region: GTP-binding protein Rab1, splice variant #status predicted <MAT2>
 F12-127/Region: translation elongation factor Tu homology <ETU>
 F18-25/Region: nucleotide-binding motif A (P-loop)
 F62-67/Region: nucleotide-binding motif B
 F124-127/Region: GTP-binding NFKD motif
 F24,25,43,124,125,127,154/Binding site: SAK/L motif
 F154-156/Region: GTP-binding SAK/L motif
 F154-156/Region: nucleotide-binding motif A (P-loop)
 F1-25,43,124,125,127,154/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #status predicted <ETU>
 F194/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted <ETU>
 F204,205/Binding site: geranyl-geranyl (Cys) (covalent) (by cdc2 kinase) #status predicted <ETU>
 Query Match 97.1%; Score 860; DB 1; Length 205;
 Best Local Similarity 84.4%; Pred. No. 1..7e-61;
 Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 Db 1 MSSMNPEVYDYLFLKLLIIGDSGVGKSCLLRADDTYTESYISTIGVDFKIRTIELDKTI 60
 Db 1 KLIQI-----ESPNVQKQIQLDRIYASEVNUK 88
 Db 61 KLIQI-----ESPNVQKQIQLDRIYASEVNUK 120

Query Match 97.1%; Score 860; DB 1; Length 205;
 Best Local Similarity 84.4%; Pred. No. 1..7e-61;
 Matches 173; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MSSMNPEVYDYLFLKLLIIGDSGVGKSCLLRADDTYTESYISTIGVDFKIRTIELDKTI 60
 Db 1 MSSMNPEVYDYLFLKLLIIGDSGVGKSCLLRADDTYTESYISTIGVDFKIRTIELDKTI 60
 Db 181 TAGGAEKSNTKIQSTPVKQSGGGCC 205

RESULT 4

TVHQP GTP-binding protein Rab1 - rat
 N;Alternate names: transforming protein ypt1 homolog
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Aug-1992 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
 C;Accession: A39963
 R;Touchot, N.; Chardin, P.; Tavitian, A.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8210-8214, 1987
 A;Title: Four additional members of the Ras gene superfamily isolated by an oligonucleotide
 A;Reference number: A39963; MUID:88068563; PMID:3317403
 A;Accession: A39963
 A;Molecule type: mRNA
 A;Residues: 1-205 <TOU>
 A;Cross-references: UNIPROT:P05711; GB:J02998; NID:9206552; PIDN:AAA42006.1; PID:9206553

RESULT 3

TWSYF

OM protein - protein search, using sw model

Run on: November 17, 2004, 14:08:55 ; Search time 40 Seconds (without alignments)
286.825 Million cell updates/sec

Title: US-09-820-003C-2
Perfect score: 886
Sequence: 1 MSSMNPEYDYLFLKLLIGDS EKSNVNLQIQTIVPKQSGGGCC 173
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Parents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A__COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6A__COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6B__COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PC7US__COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/backfilesl.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfilesl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	857	96.7	205	4 US-09-709-103-49
2	857	96.7	4	US-09-439-410A-49
3	813.5	91.8	201	2 US-08-531-525-3
4	813.5	91.8	201	2 US-08-718-270A-13
5	766.5	86.5	201	2 US-08-916-901-3
6	766.5	86.5	201	3 US-09-154-602-3
7	760.5	85.8	201	2 US-08-916-901-8
8	760.5	85.8	201	3 US-08-154-602-8
9	702.5	79.3	202	2 US-08-531-525-14
10	702.5	79.3	202	2 US-08-718-270A-14
11	595.5	67.3	227	4 US-08-248-796A-20291
12	439	49.5	215	2 US-08-531-525-10
13	439	49.5	215	2 US-08-718-270A-10
14	424	47.9	207	2 US-08-531-525-35
15	424	47.9	207	2 US-08-718-270A-35
16	418	47.2	207	2 US-08-1824-873-4
17	418	47.2	3	US-09-198-184-4
18	417.5	47.1	205	2 US-08-531-525-25
19	417.5	47.1	205	2 US-08-718-270A-25
20	403	45.5	203	4 US-08-255-920A-12
21	390	44.0	198	2 US-08-531-525-51
22	390	44.0	198	2 US-08-718-270A-51
23	366	41.3	198	2 US-08-531-525-34
24	366	41.3	194	2 US-08-718-270A-34
25	366	41.3	227	4 US-09-270-767-6812
26	360	213	4	US-09-248-796A-20293
27	334.5	37.8	214	4 US-09-270-767-33012

ALIGNMENTS

RESULT 1
US-09-709-103-49
; Sequence 49, Application US/09709103
; Patent No. 6733991
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/709,103
; CURRENT FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 49
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-709-103-49

Query Match 96.7%; Score 857; DB 4; Length 205;
Best Local Similarity 83.9%; Pred. No. 2. 2e-92; 0; Indels 32; Gaps 1;

Qy	1 MSSMNPEYDYLFLKLLIGDSVGKSCLLRFAADDTYTESYISTIGDFKRTIELDGKTI	60
Db	1 MSSMNPEYDYLFLKLLIGDSVGKSCLLRFAADDTYTESYISTIGDFKRTIELDGKTI	60
Qy	61 KLOI-----ESFNVKQWQLEIDYASENWNL	88
Db	61 KLOIWDTAGOERFRFTTSSYRGAGHIVVVDVTDQESFNVKQWQLEIDYASENWNL	120
Qy	89 LVGNKCDLTKVWVDTTAKFADSLGIPPIETSAKQNTWQSFMTMAARIKKMCPGA	148
Db	121 LVGNKCDLTKVWVDTTAKFADSLGIPPIETSAKQNTWQSFMTMAARIKKMCPGA	180
Qy	149 TAGGAERKSNVNLQIQTIVPKQSGGGCC	173
Db	181 TAGGAERKSNVNLQIQTIVPKQSGGGCC	205

RESULT 2
US-09-439-410A-49
; Sequence 49, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 191960388-B
; CURRENT APPLICATION NUMBER: US/09/439,410A

US-09-439-410A-49 CURRENT FILING DATE: 1999-11-11
 NUMBER OF SEQ ID NOS: 118 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 49 LENGTH: 205
 TYPE: PRT ORGANISM: Homo sapiens

Query Match 96.7%; Score 857, Best Local Similarity 83.9%; Pred. No. 1; Mismatches 172; Conservative 1; Mismatch

QY	1	MSMNPBPDYLKULLLIGDSGVGKSCLLR
Db	1	MSSWNPEDYDYLKULLLIGDSGVGKSCLLR
Qy	61	KIQI-----
Db	61	KIQIWTAGQERTITSSYRGHAGITW
Qy	89	LVGKNCDDLTKKVVDYTAKEFADSLGIPPF
Db	121	LVGKNCDDLTKKVVDYTAKEFADSLGIPPF
Qy	149	TAGGAEKSNVKQSTPVKQSGGSC 173
Db	181	TAGGAEKSNVKQSTPVKQAGGCC 205

RESULT 3 US-09-531-525-13

SEQUENCE 13, application US/08531525
 Patent No. 5840683

GENERAL INFORMATION:

APPLICANT: Hlaváčka, Joseph J.
 APPLICANT: Pincus, Matthew R.
 APPLICANT: No. 5840631E, John F.
 APPLICANT: Abajian, Henry B.
 APPLICANT: Kende, Andrew S.

TITLE OF INVENTION: Peptides Inhibiting
 NUMBER OF SEQUENCES: 52
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee and Winner, P.C.
 STREET: 5370 Manhattan Circle, Suitee
 CITY: Boulder
 STATE: Colorado
 COUNTRY: US
 ZIP: 80303

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version 1.0.0.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/531,525
 FILING DATE: 21-SEP-1995
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ferber, Donna M.
 REGISTRATION NUMBER: 33,878
 REFERENCE DOCKET NUMBER: 37,94
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-8080
 TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 201 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

HYPOTHETICAL: NO
 ORIGINAL SOURCE: NO
 ORGANISM: Discopyge ommata
 US-08-531-5253-13

Query Match 91.8%; Score 813.5; DB 2;
 Best Local Similarity 81.2%; Pred. No. 2.7e-87;
 Matches 164; Conservative 3; Mismatches 2;

QY 4 MNPPEYDYLFKLULIGDGSVGKSCILLRFAADDTYTESYIIS
 Db 1 MNPPEYDYLFKLULIGDGSVGKSCILLRFAADDTYTESYIIS

QY 64 I-----ESENN
 Db 61 IWDTAGQBRFRITTTSSYRGANGITIVVVDVTQBSFNN

QY 92 NKCDLTTKKVVDYTTAKEFADSIGPELETSAKNATNVE
 Db 121 NKCDLTTKKVVDYTT-KEFADSLGIPPLETSAKNATNVE

QY 152 GAEKSNVKIQSTPVKOSGGGC 173
 Db 180 GSEKSNVNIQSTPVKSSGGGC 201

RESULT 4
 US-08-718-270A-13
 ; Sequence 13, Application US/08718270A
 ; Patent No. 5910478
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Hlavka, Joseph J.
 ; APPLICANT: PinCUS, Matthew R.
 ; APPLICANT: No. 59104781e, John F.
 ; APPLICANT: Abadian, Henry B.
 ; APPLICANT: Kende, Andrew S.
 ; TITLE OF INVENTION: Peptidomimetics Inhibiting
 ; TITLE OF INVENTION: the Oncogenic Action of P211
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle, Suite 201
 ; CITY: Boulder
 ; STATE: Colorado
 ; COUNTRY: US
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.3
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/718,270A
 ; FILING DATE: 20-SEP-1996
 ; CLASSIFICATION: 514
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/531,525
 ; FILING DATE: 21-SEP-1995
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/004,091
 ; FILING DATE: 21-SEP-1995
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Peider, Donna M.
 ; REGISTRATION NUMBER: 33,878
 ; REFERENCE/DOCKET NUMBER: 78-95
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 499-8080
 ; TELEFAX: (303) 499-8089
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 201 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model
Run on: November 18, 2004, 15:49:35 ; Search time 4735 Seconds
(without alignments)

Title: US-09-820-003C-1
Perfect score: 1405
Sequence: 1 aaggatagctgagtgccg.....aaaaaaaaaaaaaaaaa 1405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gbs1:*

9: gb_gbs2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

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c	27	727.6	51.8	811	1	AJ746643	AJ746643 nx27C08-B
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c	29	723.2	51.5	1127	5	BX63467	BX63467 BX63467
c	30	721.4	51.3	919	5	BX411609	BX411609 BX411609
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c	34	714.6	50.9	994	7	CN647880	CN647880 ILMUNIGEN
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c	38	708.8	50.4	910	5	BU276678	BU276678 AGENCOURT
c	39	708.4	50.4	761	5	BU772048	BU772048 UI-H-EZL-
c	40	704.4	50.1	1105	4	BM52262	BM52262 AGENCOURT
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c	43	702	50.0	796	4	BI913092	BI913092 603179695
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RESULT 1
CR016184

DEFINITION CR616184 1927 bp mRNA, linear, HTC 21-JUL-2004
LOCUS CR616184 full-length cDNA clone CSODM010YN17 of fetal liver of Homo sapiens
(human).

ACCESSION CR616184
VERSION CR616184.1
KEYWORDS HTC; CNSL1; cDNA.

SOURCE Homo sapiens (human)

ORGANISM Bokuryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1927)
Li, W.B., Gruber, C., Jesse, J. and Polaves, D.

AUTHORS
TITLE
JOURNAL
REMARK

Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue

REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK

Submitted (20-JUL-2004) Genoscope - Centre National de Sequence :

BP 191 91006 ERY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-Oligo(dT) Primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
SOURCE

1. 1927
/organism="Homo sapiens"
'mol_type="mRNA"
'db_xref="taxon:9606"
'clone="CSDM010YN17"
'tissue_type="fetal liver"
'plasmid="pCMVSPORT_6"

ORIGIN

Query Match 85.5%; Score 1201.2; DB 3; Length 1927;
Best Local Similarity 93.0%; Pred. No. 2.5e-198;
Matches 1320; Conservative 0; Mismatches 3; Indels 97; Gaps 2;

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'plasmid="pCMVSPORT_6"

Or 1 AAGGGATAGCTGAGT-GGGCGCGCTGATGTTGTTCTAGGGACGGAGTAGGGAGA 59
Do 12 AAGGGATAGCTGAGT-GGGCGCGCTGATGTTGTTCTAGGGACGGAGTAGGGAGA 71

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 QY 180 ATGTCAGCATGATCCGAAATGATTATTCAGTACTCTGATGGACTCA 239
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 QY 360 AAGCTCAATA----- 371
 Db 372 AAGCTCAATA----- 431
 QY 372 - ----- 383
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 QY 384 ATGTTAACAGCTGCTGCGAGAAATAGTCTGTTATGCCAGTGAATGCTACAAATG 443
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 QY 684 GTGGAGGGTGCCTAAATTGCTCCATCTTCTGAGAACATGTTGGCACT 743
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 QY 804 GATCTTACCGTCTCCACAAAGTCAGGATGTAATGTTACTGCTGCTACACA 863
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 QY 924 GGTGTTAAATGATGCTGTAATCTGCTTCTGATGACGACTGTTCCCGTG 983
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 Db 1092 GTGGTGTGAAATATTTGTTGATGTTATGGCATTTAGTGTAGGTTAG 1151

RESULT 2
 CS593530 LOCUS CR593530
 DEFINITION full-length cDNA clone 1440 bp mRNA linear HTC 21-JUL-2004
 25-normalized of Homo sapiens (human).
 ACCESSION CR593530
 VERSION CR593530.1 GI:50474337
 KEYWORDS HTC; CNSIT; cDNA.
 REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jussee, J. and Polayes, D.
 SOURCE
 ORGANISM Homo sapiens (human)
 JOURNAL
 REMARK
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
 1 (bases 1 to 1440)
 2 (bases 1 to 1440)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REMARK
 Unpublished
 Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://full-length.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 Full-length cDNA libraries and normalization
 Genoscope
 Direct Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91056 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 COMMENT
 1st strand cDNA was primed with a NotI-oligo(dN) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS00C0237R06"
 /tissue="Neuroblastoma"
 /plasmid="pCMVSPORT_6",
 /
 Query Match 84.6%; Score 1188; DB 3; Length 1440;
 Best Local Similarity 93.1%; Pred. No. 4; se-156; Matches 1305; Conservative 0; Mismatches 0; Indels 97; Gaps 2;
 Matches 1305; Conservative 0; Mismatches 0; Indels 97; Gaps 2;
 QY 1 1 AAGGATAGTGTGAGTGCCTGGGTGCTGATGTTGTTAGGGACGGAGTGGGGAGAA 59
 Db 39 AAGGGATAGTGTGAGTGCCTGGGTGCTGATGTTGTTAGGGACGGAGTGGGGAGAA 98
 QY 60 CGGGTGTCTCCGGACAGGCCTATCTTCTGATGTTGCTGAGGGACGGAGTGGGGAG 119
 Db 99 CGGGTGTCTCCGGACAGGCCTATCTTCTGATGTTGCTGAGGGACGGAGTGGGGAG 158

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 Db 421 CCAAGTGAATAATGAGTCCTCAATAATGTTAACCTGGCGCAGGAAATGATCCTATG 420
 QY 481 TACTAGACTACACACACAGCAAGAAATTGCTGATTCCTGGAAATTGGAA 540
 Db 481 TACTAGACTACACACACAGCAAGAAATTGCTGATTCCTGGAAATTGGAA 540
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 Db 541 CCGTGTAAAGAATGCAACGAAATGTTGGTAGGGACAAATGTAACAGTGGCAGGAATGATCCTGGAA 540
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 Db 601 AAAGCGGAAATGGCCCGAGCAACAGCTGGCTGCTGAGAAGTCCATGTTAAATTC 660
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 QY 360 AGCTTCAATAA..... 371

ALIGNMENTS

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Sequence 10, Appli

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 Db 1221 TTCCATGATAAAGTTGAGGAGTACATCTGATGTTATGTAAGTCACTCTG 1280
 QY 1162 TGTAGAGTTAAATGGAGGTTACATCTGATGTTATGTAAGTCACTCTG 1221
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 QY 1222 ATATTTGTCGCGAGATATGTTGACACTATGTTGACAAAGACTGAG 1281
 Db 1341 ATATTTGTCGCGAGATATGTTGACACTATGTTGACAAAGACTGAG 1400
 QY 1282 ATATGTTAAATATGTTGACATGTTGAGTAAATGAA 1323
 QY 369 ATA----- 371

Db 1401 ATATGTTAAATATGTTGACTATGGAAGTAAATCAA 1442

RESULT 2

US-09-016-434-1422

Sequence 1422 Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

ZIP: 94304

ZIP: 94304

COMPUTER READABLE FORM:

COMPILER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HERENITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1422:

SEQUENCE CHARACTERISTICS:

LENGTH: 723 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9550059

US-09-016-434-1422

Query Match 33.9%; Score 476.2; DB 4; Length 723;

Best Local Similarity 84.6%; Pred. No. 7.4e-88; Matches 613; Conservative 0; Mismatches 13; Indels 99; Gaps 3;

Matches 613; Conservative 0; Mismatches 13; Indels 99; Gaps 3;

QY 129 GCGGGCTGCGCAGCAAGGAGCTGTCGTCAC 1101

Db 2 GCGGGCTGCGCAGCAAGGAGCTGTCGTCAC 1120

QY 189 ATGAACTCCGAGTATGATTTCAAGTACTCTGATGTTGCGACTCAGGGTGTGCA 188

Db 60 ATGAACTCCGAGTATGATTTCAAGTACTCTGATGTTGCGACTCAGGGTGTGCA 119

QY 249 AAGCTCTGCTCTCTTGTGTTGAGTATGATCATATACAGAACTACATGAGCA 308

Db 120 AAGCTCTGCTCTCTTGTGTTGAGTATGATCATATACAGAACTACATGAGCA 179

QY 309 ATGGTGTGGATTCAAATAAGACTATAGAGTATAGGGAAACAACTCAAGCTC 368

Db 180 ATGGTGTGGATTCAAATAAGACTATAGAGTATAGGGAAACAACTCAAGCTC 239

GenCore version 5.1.6
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On nucleic - nucleic search, using SW model
Run on: November 18, 2004, 08:12:49 ; Search time 732 Seconds
Sequence: 1 aagcgattatgtgagtgccgc.....aaaaaaa.....aaaaaaa 1405
IDENTITY_NUC: 100%
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : N_Geneseq_23Sep04: *

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- 2: geneseqn1990s: *
- 3: geneseqn2000s: *
- 4: geneseqn2010s: *
- 5: geneseqn2001bs: *
- 6: geneseqn2002as: *
- 7: geneseqn2002bs: *
- 8: geneseqn2003as: *
- 9: geneseqn2003bs: *
- 10: geneseqn2003cs: *
- 11: geneseqn2003ds: *
- 12: geneseqn2004as: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
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3	1201.2	85.5	8131	10	ADE54064		ABX13973;
4	1200.2	85.4	2528	3	ACG0009		ABX13973;
5	1191.2	84.8	1415	10	ADB61467		DT 19-FEB-2003 (first entry)
6	1189.6	84.7	1415	10	ADB11443		XX
7	1179.2	83.9	8137	12	AD161639		DE Human Ras-like protein cDNA.
8	1103.6	78.5	2257	10	ADP53080		KW Human; gene; ss; Ras-like protein; Ras; low molecular weight; LMW; small regulatory guanine nucleotide-binding protein; GTP-binding protein; apoptosis; AIDS; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; myelodysplastic syndrome; aplastic anaemia; ischaemic injury; myocardial infarction; stroke; toxin-induced disease; alcohol-induced liver damage; cirrhosis; wasting disease; cachexia; viral infection; hepatitis; osteoporosis; cell proliferation; cancer; leukaemia; inflammation; allergy; asthma; atherosclerosis; diabetes mellitus; rheumatoid arthritis; therapeutic; transgenic; pharmacogenomic analysis; genotype; antisense; gene therapy.
9	1029	73.2	1193	5	AAS83860		KW XX
10	994.6	70.8	1545	12	ADM6955		OS Homo sapiens.
11	817.2	58.2	1874	10	ADX13974		PH Key
12	684.4	48.7	4819	12	ADJ32289		FT CDS
13	533.2	36.0	604	10	ADB11343		FT / *tag= a / product= "Ras-like protein"
14	506	36.0	506	10	ADP4823		FT
15	476.2	33.9	723	6	ABK83978		XX US2002142382-A1.
16	476.2	33.9	723	10	ADB11463		PD 03-OCT-2002.
17	476.2	33.9	723	10	ACG56824		XX
18	476.2	33.9	723	12	ADT56620		PF 29-MAR-2001; 2001US-00820003.
19	467	33.2	487	4	AAT11818		XX
20	467	33.2	487	4	ABP5312		PR 29-MAR-2001; 2001US-00820003.
21	467	33.2	487	4	AAT33136		XX DR WPI; 2003-102518/09.

ALIGNMENTS

c	22	467	33.2	487	4	ABX43096	Abx43096 Human bre
c	23	467	33.2	487	4	ABA23276	Abx23276 Probe #17
c	24	467	33.2	487	4	AK027239	AK027239 Human bra
c	25	467	33.2	487	4	AK01783	AK01783 Human bra
c	26	467	33.2	487	4	AB56815	AB56815 Human liv
c	27	467	33.2	487	5	AK01752	AK01752 Probe #17
c	28	467	33.2	487	6	AB90172	Abx0172 Human gen
c	29	427.8	30.4	497	10	ADD33239	Add33239 Mouse mit
c	30	411.4	29.3	615	10	ABD61462	Abx61462 Amyloid b
c	31	411.4	29.3	615	10	ABD61442	Abx61442 DNA encod
c	32	358.4	25.5	618	10	ADP53200	Adp53200 Primary r
c	33	341.8	24.3	618	9	ACI17697	ACI17697 Human adu
c	34	337.2	24.0	353	8	ABX40262	Abx40262 Bovine ES
c	35	333.4	23.7	335	3	AAC06621	Ac06621 Human sec
c	36	331.6	23.6	331	3	ADD33240	Add33240 Mouse mit
c	37	314.8	22.4	427	8	ABX43746	Abx43746 Bovine ES
c	38	314.6	22.4	483	9	ACI15492	ACI15492 Human adu
c	39	314.6	21.4	482	6	ADP46733	Adp46733 Human Ras
c	40	280.4	20.0	459	9	ACI17419	ACI17419 Human inf
c	41	264	18.8	405	5	ABV14061	Abv14061 Human pro
c	42	262	18.6	448	5	ABV44007	Abv44007 Human pro
c	43	262	18.6	448	5	ABV35165	Abv35165 Human pro
c	44	261	18.6	290	6	ABL75210	AbI75210 Corn tass
c	45	232.8	16.6	241	4	AAE17849	Aae17849 Human bre

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2004, 09:13:54 ; Search time 6027 Seconds
 (without alignments)
 11024.063 Million cell updates/sec

Title: US-09-820-003c-1

Perfect score: 1405

Sequence: 1 aagcgattatcgatcgcc.....aaaaaaaaaaaaaaaaa 1405

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : GenEmbl:*

1: gb_bat:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGMENTS

1: HSM06623

2: HSM06623

3: HSM06623

4: HSM06623

5: HSM06623

6: HSM06623

7: HSM06623

8: HSM06623

9: HSM06623

10: HSM06623

11: HSM06623

12: HSM06623

13: HSM06623

14: HSM06623

15: HSM06623

16: HSM06623

17: HSM06623

18: HSM06623

19: HSM06623

20: HSM06623

21: HSM06623

22: HSM06623

23: HSM06623

24: HSM06623

25: HSM06623

26: HSM06623

27: HSM06623

28: HSM06623

29: HSM06623

30: HSM06623

31: HSM06623

32: HSM06623

33: HSM06623

34: HSM06623

35: HSM06623

36: HSM06623

37: HSM06623

38: HSM06623

39: HSM06623

40: HSM06623

41: HSM06623

42: HSM06623

43: HSM06623

44: HSM06623

45: HSM06623

RESULT 1

HSMD06623

LOCUS HSM06623 1625 bp mRNA linear PRI 15-JUL-2003

DEFINITION Homo sapiens mRNA; cDNA DKFZp86E08159 (from clone DKFZp86E08159); complete cds.

ACCESSION BX571747

VERSION BX571747.1

KEYWORDS G1:33096734

SOURCE

ORGANISM Homo sapiens (human)

Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo; Bathyrotora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo.

1 (bases 1 to 1625)

REFERENCE

AUTHORS Koehrer,K., Bever,A., Meves,H.W., Weil,B., Amid,C., Osanger,A.,

CONTRM

TITLE Submitted (16-JUL-2003) MIPS, Ingolstaedter Landstr.1, D-8564 Neuherberg, GERMANY

JOURNAL

COMMENT

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Heinrich-Heine-Universität, Düsseldorf (Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp86E08159) is available at the RZPD in Berlin. Please contact RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mpis.gsfc.nasa.gov/cDNA/>.

FEATURES

Source

1. -1625

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="Raxxon:9606"

/map="2p14"

/clone="DKFZp86E08159"

/tissue_type="human colon endothelial primary cell culture"

/clone_Lib="686 (synonym: hlcc3). Vector psport1_SfiI; host DH10B; sites Sfi1A + Sfi1B"

/dev_stage="adult"

1. -1625

/gene="DKFZp86E08159"

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1277	90.9	1625	HSM06623
2	1219	86.8	1433	BC000905
3	1179.2	83.9	8137	AR454534
4	1103.6	78.5	2257	AXT13964
5	1103.6	78.5	2257	AK055927
6	1052.6	74.9	1444	BC002077
7	1044	74.3	1208	HSM060023
8	1036.2	73.8	2819	AK129477
9	1028.2	73.2	1425	BC006662
10	1013.2	72.1	1428	MMY01
11	955	68.6	2686	AF226873
12	820.6	58.4	292895	AC123143
13	817.2	58.2	204230	AC007318
14	797.4	56.8	329753	AC0096701
15	777.8	55.2	327906	AC117841
16	741.4	52.8	203071	AL606522
17	727.8	51.8	243263	AC135510
18	697.2	49.6	327906	AC117841
19	687.6	48.9	116614	AL512349

CDS

184. .801

/gene="DKFZp686B08159"

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GenCore version 5.1.6

Run on: November 17, 2004, 14:17:35 ; Search time 140 Seconds
(without alignments)
437,601 Million cell updates/sec

Title: OM protein - protein search, using sw model

Perfect score: US-09-820-003A-2

Sequence: 1 MSSMNPYDYLKULLLGDS ERSNVKIQSTPKQSGGGC 173

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first: 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTNS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_N_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_N_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US11_N_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US12_N_PUB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

US-09-820-003A-2

; Sequence 2, Application US/09820003A

; Patent No. US2002142382A1

; GENERAL INFORMATION:

; APPLICANT: MERKULOV, Gennady et al.

; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS, AND USES THEREOF

; TITLE OF INVENTION: NUCICIC ACID MOLECULES ENCODING RAS-LIKE PROTEINS, AND USES THEREOF

; TITLE OF INVENTION: PROTEINS, AND USES THEREOF

; FILE REFERENCE: CL00116

; CURRENT APPLICATION NUMBER: US/09/820, 003A

; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSBQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 173

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-820-003A-2

Query Match 100.0% ; Score 886; DB 9

Best Local Similarity 100.0%; Preq. No. 3 9e-7

Matches 173; Conservative 0; Mismatches 0

Result No.	Score	Query Match Length	DB ID	Description
1	886	100	0	173 9 US-09-820-003A-2
2	886	100	0	173 9 US-10-112-944-292
3	860	97	1	222 9 US-09-820-003A-4
4	857	95	1	205 16 US-10-804-491-49
5	812.5	91	7	201 17 US-10-471-411-6
6	792.5	89	4	169 17 US-10-471-411-2
7	768.5	86	7	224 9 US-09-925-298-466
8	768.5	86	7	224 14 US-10-102-806-466
9	766.5	86	5	201 9 US-09-967-736-3
10	766.5	86	5	201 14 US-10-291-172-193
11	766.5	86	5	201 15 US-10-221-278-193
12	766.5	86	5	201 16 US-10-408-765A-1596
13	766.5	86	5	201 17 US-10-471-411-4

E HUMAN RAS-LIKE		B RAS-LIKE	
Sequence	5, Appl	Sequence	5, Appl
Sequence	2387, Ap	Sequence	7, Appl
Sequence	7, Appl	Sequence	6241, Ap
Sequence	8, Appl	Sequence	8, Appl
Sequence	10551,	Sequence	186767,
Sequence	82411, Ap	Sequence	47782, A
Sequence	47782, A	Sequence	41359, A
Sequence	41359, A	Sequence	42447, A
Sequence	42447, A	Sequence	56916, A
Sequence	186767,	Sequence	362779,
Sequence	362779,	Sequence	45295, A
Sequence	45295, A	Sequence	318489,
Sequence	318489,	Sequence	47497, A
Sequence	47497, A	Sequence	60367,
Sequence	60367,	Sequence	67150, A
Sequence	67150, A	Sequence	186764,
Sequence	186764,	Sequence	44811, A
Sequence	44811, A	Sequence	123354,
Sequence	123354,	Sequence	318493,
Sequence	318493,	Sequence	60163, A
Sequence	60163, A	Sequence	624895, A
Sequence	624895, A	Sequence	61060, A
Sequence	61060, A	Sequence	318496,
Sequence	318496,	Sequence	186768,
Sequence	186768,	Sequence	7703, Ap
Sequence	7703, Ap	Sequence	200936,
Sequence	200936,	Sequence	136472,
Sequence	136472,	Sequence	331973,
173;			
s	0;	Gaps	0;

RESULT 2
 US-10-112-944-292
 ; Sequence 292, Application US/1011294
 ; Publication No. US20040048249A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yang, Y. Tom
 ; APPLICANT: Yang, Yongzhong
 ; APPLICANT: Weng, Gezhi
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghosh, Malabika
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Zhao, Qing A.
 ; TITLE OF INVENTION: No. US20040048249A1 Nucleic Acids and
 ; TITLE OF INVENTION: Secreted Polypeptides
 ; FILE REFERENCE: 805A
 ; CURRENT APPLICATION NUMBER: US/10/112,944
 ; CURRENT FILING DATE: 2002-03-28
 ; CURRENT APPLICATION NUMBER: US 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US 09/491,404
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: US 09/496,914
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: US 09/515,126
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: US 09/519,705
 ; PRIOR FILING DATE: 2000-03-07
 ; PRIOR APPLICATION NUMBER: US 09/540,217
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: US 09/552,929
 ; PRIOR FILING DATE: 2000-04-18
 ; PRIOR APPLICATION NUMBER: US 09/577,408
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 924
 ; SOFTWARE: pt_PL_genes Version 5.0
 ; SEQ ID NO 292
 ; LENGTH: 173
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-112-944-292

Query Match 100.0%; Score 886; DB 15; Length 173;
 Best Local Similarity 100.0%; Pred. No. 3.9e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 173; Conservative 0;

QY 1 MSSMNPEVDYLKULLIGSGVGKSCLLRFADDTYTESYISTIGDPFKIRTELDKTI 60
 Db 1 MSSMNPEVDYLKULLIGSGVGKSCLLRFADDTYTESYISTIGDPFKIRTELDKTI 60

QY 61 KLOQESFNNVKQWIKQBDIYRASENVNKLUVKGKCDLTTRKVDYTTAKEFADSLGIPPLE 120
 Db 61 KLOQESFNNVKQWIKQBDIYRASENVNKLUVKGKCDLTTRKVDYTTAKEFADSLGIPPLE 120

QY 121 TSAKNATNVEQSFNTMAARIKKGPGTAGAEKSNVKIQTPIVKOSGGCC 173
 Db 121 TSAKNATNVEQSFNTMAARIKKGPGTAGAEKSNVKIQTPIVKOSGGCC 173

RESULT 3
 US-09-820-003A-4
 ; Sequence 4, Application US/09820003A
 ; Patent No. US2002042382A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERKULOV, Gennady et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
 ; TITLE OF INVENTION: PROTEINS, AND USES THEREOF

Query Match 97.1%; Score 860; DB 9; Length 222;
 Best Local Similarity 84.4%; Pred. No. 1.8e-75; Mismatches 0; Indels 32; Gaps 1;
 Matches 173; Conservative 0;

QY 1 MSSMNPEVDYLKULLIGSGVGKSCLLRFADDTYTESYISTIGDPFKIRTELDKTI 60
 Db 18 MSSMNPEVDYLKULLIGSGVGKSCLLRFADDTYTESYISTIGDPFKIRTELDKTI 77

QY 61 KLOI-----ESPNVVKQWIKQBDIYRASENVNKLU 88
 Db 78 KLOIWDTAGQERFRTITSYRGHGIIVVVDVTDQESFNNVKQWIKQBDIYRASENVNKLU 137

QY 89 LVNKCDLTTRKVDYTTAKEFADSLGIPPLETSAKNATNVEQSFNTMAAEIKKRMGPG 148
 Db 138 LVNKCDLTTRKVDYTTAKEFADSLGIPPLETSAKNATNVEQSFNTMAAEIKKRMGPG 197

QY 149 TAGGAEKSNVKIQTSPVKOSGGCC 173
 Db 198 TAGGAEKSNVKIQTSPVKOSGGCC 222

RESULT 4
 US-10-804-491-49
 ; Sequence 49, Application US/1080491
 ; Publication No. US2004180375A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cismowski, Mary
 ; APPLICANT: Duzic, Emir
 ; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
 ; FILE REFERENCE: 60388-A-PCM-US
 ; CURRENT APPLICATION NUMBER: US/10/804,491
 ; CURRENT FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: US/09/709,103
 ; PRIOR FILING DATE: 2000-11-08
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 49
 ; LENGTH: 205
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-10-804-491-49

Query Match 96.7%; Score 857; DB 16; Length 205;
 Best Local Similarity 83.9%; Pred. No. 3.3e-75; Mismatches 0; Indels 32; Gaps 1;
 Matches 172; Conservative 1;

QY 1 MSSMNPEVDYLKULLIGSGVGKSCLLRFADDTYTESYISTIGDPFKIRTELDKTI 60
 Db 1 MSSMNPEVDYLKULLIGSGVGKSCLLRFADDTYTESYISTIGDPFKIRTELDKTI 60

QY 61 KLOI-----ESPNVVKQWIKQBDIYRASENVNKLU 88
 Db 61 KLOIWDTAGQERFRTITSYRGHGIIVVVDVTDQESFNNVKQWIKQBDIYRASENVNKLU 120

QY 89 LVNKCDLTTRKVDYTTAKEFADSLGIPPLETSAKNATNVEQSFNTMAAEIKKRMGPG 148
 Db 121 LVNKCDLTTRKVDYTTAKEFADSLGIPPLETSAKNATNVEQSFNTMAAEIKKRMGPG 180

QY 149 TAGGAEKSNVKIQTSPVKOSGGCC 173
 Db 181 TAGGAEKSNVKIQTSPVKOSGGCC 205